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GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on:	January 24, 2003, 18:40:04 ; Search time 2232 Seconds (without alignments) 123.353 Million cell updates/sec
Title: Perfect score: Sequence:	US-09-771-009-1 90 1 NFDLLKLAGDVEŠNPGP 17
Scoring table:	BLOSUM62 Xgapop 10.0 , Xgapext 0.5 Xgapop 10.0 , Ygapext 0.5 Fgapop 6.0 , Fgapext 7.0 Delop 6.0 , Delext 7.0
Searched:	16154066 seqs, 8097743376 residues
Total number of	Total number of hits satisfying chosen parameters: 32308132
Minimum DB seq length: 0 Maximum DB seq length: 20	Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Listing first 45 summaries

Command line parameters:
-MODEL-frame+_D2n_model -DEV=xlp
-Model-frame+_D2n_model -DEV=xlp
-D6-cgn2_L/USPTO_spool/US09771009/runat_22012003_140101_18469/app_query.fasta_1.199
-D8-EST -QFWT=fastap -SUFFIX=rst -MINNATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-USTFWT=pto -NORM=ext -HEAPEIXE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771009_@CGN_1_1_776_@runat_22012003_140101_18469 -NCPU=6 -ICPU=3
-NO_XNPXY -NO_MMAP -LARGEORERY -REG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN TIMEOUT=30 -THERBALS=1 -XARAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : EST:*

: em_esthum:*

: em_esthum:*

: em_esthun:*

: em_esthu:*

: em_esthu:*

: em_esthi:*

: em_esth

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		00000000000000000000000000000000000000	758 356 356 356 522 522 523 326 326 326 326 427 451 451 551 859 859 859 859 859 859 850 859 850 850 850 850 850 850 850 850 850 850	11777777777777777777777777777777777777	AQ653827 AQ651117 AQ056511 AZ157346 AZ157346 AZ156841 AZ156841 AZ20518 AZ30518 AZ301518 AZ301518 AZ30155 AZ301615 AZ301187 BH842561 BH842561 BH194419 BH194877	AQ653827 AQ651117 AQ651117 AQ15385 AZ157335 AZ15684 AZ15684 AZ15684 AZ194671 AQ908490 AZ902518 AQ908490 AZ302155 AQ445296 AQ3010615 BH8452561 BH8464419	Sheared SSTanted SP20024 P 20024 SP 20024 SP 20024 SP 20024 SP 20026 GSSTC024 GSSTC034 GSSTC034 GSSTC034 GSSTC034 TC3 53JJ TC3 53JJ TC3 58G1 TC3 58G1
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RESULT 1 AQ653827/c LOCUS AQ653827 TS8 bp DNA linear GSS 22-JUN-1999 DEFINITION Sheared DNA-1E19.TF Sheared DNA Trypanosoma brucei genomic clone Sheared DNA-1E19. DNA sequence. ACCESSION AQ653827 AQ653827 GI:5147013 KEYWORDS Trypanosoma brucei. ORGANISM Trypanosoma brucei. ORGANISM Trypanosoma brucei. Trypanosoma brucei Trypanosoma. Trypanos

ALIGNMENTS

MD 20850, USA

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/organism="Trypanosoma bruce;"
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/clone_lib="Sheared DNA-18J9"
/clone_lib="Sheared at The Insertation of Genomic DNA isolated from a cloned population of Trypanosoma bruce; (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb).
The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C.
(Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University
                                                                                                                              Email: nelsayed@tigr.org

Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared

DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: Ml3-Forward
class: shotgun
                                                               9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                     Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                              Location/Qualifiers
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/note="Vector: pUC18: Site_1: SmaI; Constructed at The Institute for Cenomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (approx 2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Waking small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
         Determination of clone end sequences from Trypanosoma brucei GUTat
10.1 sheared DNA library
Unpublished (1999)
Other_GSSs: Sheared DNA-1E19.TR
Contact: Najib M. E1.Sayed
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Email: nelsayed@tigr.org
Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
DNA library constructed at TIGR. Clones will be available for
distribution through ATCC. Sheared DNA end sequences search page:
http://www.tigr.org/tdb/mdb/tdb/.
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1 (bases 1 to 536)

Bl-Sayed, W., Zhao, H., Gill, S., Suh, E., Malek, J., Fujii, C., Gerrard, C., Leech, V., de Jong, P., Ullu, E., Melville, S., Donelson, J., Fraser, C. and Adams, M.

Determination of clone end sequences from Trypanosoma brucei GUTat 10.1 sheared DNA library Oupublished (1999)

Other_GSSs: Sheared DNA-18J9.TR
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Bukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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Matches:
Conservative:
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/strain="TRED27/4 GUTat 10.1"
/db_xref="taxon:5691"
/clone="Sheared DNA-1E19"
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Fraser, C. and Adams, M.
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AQ651117.1 GI:5144303
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57.00
86.67%
73.33%
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369 bp DNA linear GSS 09-JAN-2001 GSSTC04731 Trypanosoma cruzi random genomic library Trypanosoma AQ903690
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Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

1 (bases 1 to 369)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery
formome Res. 10 (12), 1996-2005 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               On Sep 14, 2000 this sequence version replaced gi:9374387.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    San Martin)
Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24
CP(1650) San Martin, Prov. de BS AS. Argentina
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132 g
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516 bp DNA linear GSS 29-AUG-2000 SP_0024_Al_C05_T7 Strongylocentrotus purpuratus, purple sea urchin, clone plate=24 Col=9 Row=E, DNA sequence.
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/clone_lib="Strongylocentrotus purpuratus, purple sea
/rohin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
DH108"
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/clone=lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm apenomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
                                                                                                                                                   2 others
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Davision of Biology 156-29
California Institute of Technology
Pasadena California 91125, USA
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Location/Qualifiers
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Seq primer: T7
Class: BAC ends
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                                                                                                                                                   101 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ157346.1 GI:8309947
                                                                                                                                                 104 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: (626) 395-8421
Fax: (626) 793-3047
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                                                                                                                                                                                                                                                                                                                                range
                             Email: dsanchez@iib unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                          /organism="Trypanosoma cruzi"
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/db_cre="taxon:5693"
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/orlore="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 kb ran;
was gel purified and cloned into the dephosphoryated
Hincil site of the vector"
3 a 101 c 100 g 75 t
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Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinoidea; Eucechinoidea; Echinoidea; Etrongylocentrotidae; Strongylocentrotidae; Strongylocentrotus.
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additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
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California Institute of Technology
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-771-009-1 (1-17) x AQ903690 (1-369)
Tel: 54-11-4580-7255 ext 309
Fax: 54-11-4752-9639
                                                                                                                                                              Location/Qualifiers
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AZ157335.1 GI:8309936
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Fax: (626) 793-3047
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Class: shotgun.
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AZ157335
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δŏ g us-09-771-009-1.rst

LOCUS

RESULT 6 AZ156841

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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/clone="11b="
                                                                                                                                                                                                                                                                                                                     El-Sayed,N., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C., Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melviile,S., Donelson,J., Fraser,C. and Adams,M.

Praser,C. and Adams,M.

Determination of clone end sequences from Trypanosoma brucei TREU 927/4 Pl library

Unpublished (1999)

Cher_GSSS: 927Pl-15E10.TV

Contect: Najib M. El-Sayed

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0200
                            AQ639839 57P1 Trypanosoma brucei genomic clone 927P1-15E10,
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SP_1028_A2_G12_T7A Strongylocentrous purpuratus, purple sea urchin sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=1028 Col=24 Row=M, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: nelsayed@tigr.org
For clone/filter availability, please contact Sara Melville
(smilo@mole.bio.cam.ac.uk). Pl end sequences search page:
http://www.tigr.org/tdb/mdb/tbdb/.
Seq primer: SP6
Class: Pl ends.
                                                                                                                                                                                                                                                        Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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1 (bases 1 to 573)
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urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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Mantanon, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.
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Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
20402566
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Strongylocentrotus purpuratus
Eukaryota, Metazoa; Echinodemata; Eleutherozoa; Echinodea; Euchinoidea; Echinoidea; Echinoidea; Echinoidea; Echinoidea; Strongylocentrotidae; Strongylocentrotus.
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/db_xref="taxon:7668"
/clone="Plate=49 Col=10 Row=N"
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                                                                                                                                                                                                                           4 LeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
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                            Conservative:
Mismatches:
Indels:
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     Matches:
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California Institute of Technology
Pasadena California 91125, USA
Tel: (626) 395-8421
Fax: (626) 793-3047
Email: acameron@caltech.edu
                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 522.
Location/Qualifiers
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Plate: 49 row: N column: 10
Seq primer: T7
                                                                                                                                                                    US-09-771-009-1 (1-17) x AZ157346 (1-516)
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AZ156841.1 GI:8309441
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JOURNAL MEDLINE COMMENT

TITLE

Query Match:

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BASE COUNT ORIGIN

FEATURES

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Score:

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326 bp DNA linear GSS 09-JAN-2001 GSSTC09943 Trypanosoma cruzi genomic clone G4113, DNA sequence.
AQ904204
                                                                                                                                                                                                                                                                                                                                                                                                                  range
                                                                                       Email: dsanchez@iib.unsam.edu.ar Sequences were basecalled with phred and vector was masked with crossmatch (see http://genome.washington.edu). Sequences were then trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma; Schizotrypanum.

Trypanosoma; Schizotrypanum.

T (bases 1 to 358.)

Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.

A random sequencing approach for the analysis of the trypanosoma cruzi general structure. large gene and repetitive DNA families, and gene date and secovery

Genome Res. 10 (12), 1996-2005 (2000)
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BS AS. Argentina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24 CP(1650) San Martin, Prov. de BS AS. Argentina Tel: 54-11-4580-7255 ext 309 Fax: 54-11-4752-9639
                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Trypanosoma cruzi random genomic library"
/cell_type="epimastigote"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb was gel purified and cloned into the dephosphoryated HincII site of the vector"
76 c 81 g 78 t
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Indels:
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/organism="Trypanosoma cruzi"
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Matches:
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Seq primer: T7
                                                                                                                                                                                                                                                                                       /strain="CL-Brener"
/db_xref="taxon:5693"
/clone="G57N10"
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Av. Gral Paz entre Albarellos
CP(1650) San Martin, Prov. de
Tel: 54-11-4580-7255 ext 309
Fax: 54-11-4752-9639
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84.62$
69.23$
58.89$
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Trypanosoma cruzi
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TITLE
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"Coganism="Strongylocentrotus purpuratus"

"Ab_xref="taxon:7668"

"Clone="plate=1028 Col=24 Row=M"

/Clone_lib="Strongylocentrotus purpuratus, purple sea

"Chin, sperm genomic BAC library"

/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli

DH108"
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                                                                               Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 781)

Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray
, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aguaro, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi apnome: general structure, large gene and repetitive DNA families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
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San Martin)
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cruzi genomic clone G57N10, DNA sequence.
A2302518
                                                                                                                                                                                                              sea urchin genome project: Sequence scan, virtual map, and
                               Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
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Bukaryota; Euglanozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 288)
                                                                                                                                                                                                                           additional resources
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)
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Division of Biology 156-29
California Institute of Technology
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Location/Qualifiers
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              Strongylocentrotus purpuratus.
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Fax: (626) 793-3047
Email: acameron@caltech.edu
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Contact: Sanchez D.O.
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Best Local Similarity:
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AUTHORS
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A2302155 359 bp DNA linear GSS 09-JAN-2001 GSSTC12269 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G1608, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: dsanchez@iib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="CL-Brener"
/db_xref="taxon:5693"
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/cell_type="epimastigote"
/cell_type="epimastigote"
/note="Vector: pBS(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb ran was gel purified and cloned into the dephosphoryated Hincil site of the vector"

59 a 101 c 100 g 89 t
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
I (bases 1 to 359)
Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Instituto de Investigaciones Biotecnologicas (Univ. Nac.
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                                                                          US-09-771-009-1 (1-17) x AQ908490 (1-326)
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1. .359
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GSS.
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Trypanosoma cruzi
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Class: shotgun.
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Trypanosoma cruzi.
Eukaryota, Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 326)
Aguero,F., Verdun,R., Frasch,A.C.C. and Sanchez,D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome; general structure, large gene and repetitive DNA families, and gene discovery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral San Martin)
Av. Gral Paz entre Albarellos y Constituyentes, INTI edificio 24 (201650) San Martin, Prov. de BS AS. Argentina
Tel: 54-11-4580-7255 ext 309
Fax: 54-11-4752-9639
Email: dsanchez@lib.unsam.edu.ar
           /clone="G4I13"
/clone="Trypanosoma cruzi random genomic library"
/clone_lib="Trypanosoma cruzi random genomic library"
/coll_rype="epimastigote"
/cot="Vector: pB8(-) (Stratagene); T. cruzi DNA was randomly sheared using a nebulizer and the 1 to 2 Kb was gel purified and cloned into the dephosphoryated HincII site of the vector"
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Mismatches:
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Matches:
Conservative:
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/strain="CL-Brener"
/db_xref="taxon:5693"
/clone="G29113"
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88 c 87 g 66
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 /db_xref="taxon:5693"
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Class: shotgun.
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AUTHORS
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/strain="CL-Brener" // strain="CL-Brener" // strain="CL-Brener" // db_xref="taxon:5693" // clone="GAZN24" // clone="Ib="Trypanosoma cruzi random genomic library" // cell_type="epimastigote" // cell_type="epimastigote" // cell_type="epimastigote" // cell_type="period of clone colone colone
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Dukaryotis, Englenozoa; Kinetoplastida; Trypanosomatidae;
Dukaryotis, Englenozoa; Kinetoplastida; Trypanosoma; Schizotrypanum.
1 (bases 1 to 427)
A quero.F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA Genome Res. 10 (12), 1996-2005 (2000)
                                                                                                                                                                                                                                                                                                                                                        Av. Gral Faz entre Albarellos y Constituyentes, INTI edificio 24 CP(1650) San Martin, Prov. de BS AS. Argentina Tel: 54-11-4580-7255 ext 309 Fax: 54-11-4752-9639
                    Trypanosoma; Schizotrypanum.

I (bases 1 to 418)

Aquero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
A random sequencing approach for the analysis of the trypanosoma cruzi genome: general structure, large gene and repetitive DNA families, and gene discovery and gene fascovery (2000)

Genome Res. 10 (12), 1996-2005 (2000)

On Sep 14, 2000 this sequence version replaced gi:9378713.

Contact: Sanchez D.O.
                                                                                                                                                                                                                                                                                                                 Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
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Best Local Similarity:
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GSSTC01571 Trypanosoma cruzi random genomic library Trypanosoma cruzi genomic clone G4C3, DNA sequence.
A0445296.3 GI:10138167
GSS.
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/cell_type="epimastigote"
/note="Vector: pBS(-) (Stratagene): T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphoryated
HincII site of the vector"
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AQ910615 AQ910615 GI:10136876 GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 54-11-4752-9639
Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
                                                                                                                                                                                                                                                                                                                                   Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
Aguero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
Arandom sequencing approach for the analysis of the trypanosoma
cruzi genome: general structure, large gene and repetitive DNA
families, and gene discovery
Genome Res. 10 (12), 1996-2005 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   On Sep 14, 2000 this sequence version replaced gi:9375285.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
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Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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/db_xref="taxon:5693"
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Class: shotgun.
Location/Qualifiers
1. .379
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ORIGIN
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COMMENT
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TITLE
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AQ910615
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Search completed: January 24, 2003, 20:16:20 Job time : 2236 secs

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protein

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Sequence:

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Sequence 5, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Method of Producing Chimeric Protein CURRENT APPLICATION NUMBER: US/08/844,045C
CURRENT FILING DATE: 1997-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
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US-08-778-570B-7

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US-08-472-3584-1

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US-08-687-892-6

US-08-387-892-6

US-08-387-892-6

US-09-294-384B-6

US-08-177-079-6

US-08-177-079-6

US-08-177-079-5

US-08-177-079-5

US-08-177-079-5

US-08-177-079-5

US-08-177-079-5

US-08-177-079-5

US-08-483-119

US-09-100-546-19

US-09-100-546-19

US-09-100-546-19

US-09-100-546-19

US-09-100-546-19

US-09-100-15-19

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US-09-100-11-19

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US-08-177-079-8

US-08-177-079-8

US-08-485-938A-30

US-08-485-938A-30

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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-08-844-045C-14
; Sequence 14, Application US/08844045C
; Patent No. 6232099
; GENERAL INPORMATION:
APPLICANT: Scottish Crop Research Institute
; TITLE OF INVENTION: Method of Producing Chin
                                                                                                                                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Foot-and-mouth disease virus
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  US-08-844-045C-14
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Best Local Similarity:
  NAME/KEY: CDS
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LENGTH: 60
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-MODEL-frame+_p2n.model -DEV=Xlp
-QODEL-frame+_p2n.model -DEV=Xlp
-QO-Cqgn2_1/USPTO_Spool/US09771009/runat_22012003_140101_18519/app_query.fasta_1.199
-QO-Cqgn2_1/USPTO_Spool/US09771009/runat_22012003_140101_18519/app_query.fasta_1.199
-QO-Cqu2_d_Gatents_NA -QFWT=fastap -SUFFIX=ni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=Eptt -THR_MAX=100 -THR_MIN-0 -ALIGN=15
-MODE-LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER=US0971009_@CGN_1_1_31_@runat_22012003_140101_18519 -NCPU=6 -ICPU=3
-NO_MAYR -NO_MAMP -LARGEQUERY -NCG_SCORES=0 -WAIT -LONGIGG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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Sequence 16, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 11, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 25, Appl
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Appl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd
                                                          nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-844-045C-14
US-08-844-045C-15
US-08-844-045C-12
US-08-091-219-1
US-09-293-549-11
US-08-276-968A-21
US-08-276-968A-21
US-08-276-968A-21
US-08-276-968A-21
US-08-276-968A-21
US-08-276-968A-21
US-08-278-357-3
US-08-778-8
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Maximum Match 100%
Listing first 45 summaries
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, Ygapext
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Match Length
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US-08-844-045C-16

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; NAME/KEY: CDS
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US-09-091-219-1
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NAME/KEY: CDS

LOCATION: (1)..(183)

US-08-844-045C-18
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Best Local Similarity:
Query Match:
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; Patent No. 623209
; GENERAL INFORMATION:
; APPLICANT: Scottish Crop Research Institute
; TITLE OF INVENTION: Method of Producing a Chimeric Protein
; CURRENT APPLICATION UNMBER: US/08/844,045C
; CURRENT PILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 197
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 12
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Scottish crop Research Institute

TITLE OF INVENTION: Method of Producing Chimeric Protein

FILE REFERENCE: Method of Producing a Chimeric Protein

CURRENT APPLICATION NUMBER: US/08/844,045C

CURRENT FILING DATE: 1997-04-18

NUMBER OF SEQ ID NOS: 19

SEQ ID NO 16

LENGTH: 60
                                                                                                                                                                                         TYPE: DNA ORGANISM: Foot-and-mouth disease virus FEATURE: OTHER INFORMATION: Description of Unknown Organism:NIL
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Matches:
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Sequence 16, Application US/08844045C
Patent No. 6232099
                                                                                                                                                                                                                                                                                                                                    9.79e-08
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; LOCATION: (1)..(81)
US-08-844-045C-12
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Best Local Similarity:
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Best Local Similarity:
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US-08-844-045C-12

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; NAME/KEY: CDS ; LOCATION: (1) US-08-844-045C-16

Alignment Scores:

Pred. No.:

Score:

Query Match:

Sequence 18, Application US/08844045C

S-08-844-045C-18

Alignment Scores:

Pred. No.:

Query Match:

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TYPE: DNA

FEATURE:

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136 AATTTTGACCTTCTCAAGTTGGCGGGAGACGTCGAGCTCCAACCCTGGG 183
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GENERAL INFORMATION:
APPLICANT: Scottish Crop Research Institute
TTLE OF INVENTION: Method of Producing Chimeric Protein
FILE REFERENCE: Method of Producing a Chimeric Protein
CURRENT APPLICATION NUMBER: US/08/844,045c
CURRENT FILING DATE: 1997-04-18
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                       183
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; GENERAL INFORMATION:
APPLICANT: STUDDERT, Michael J.
APPLICANT: STUDDERT, Michael J.
APPLICANT: CREB, Brendan S.
APPLICANT: CRAB, Brendan S.
TITLE OF INVENTION: EQUINE RHINOVIRUS 1 PROTEINS
FILE REFERENCE: 040268/0151
CURRENT APPLICATION NUMBER: US/09/091,219
CURRENT APPLICATION NUMBER: PCT/ANU96/00815
EARLIER APPLICATION NUMBER: PCT/ANU96/00815
EARLIER APPLICATION NUMBER: AU PN7201
EARLIER APPLICATION NUMBER: AU PN7201
SEQ ID NOS: 25
SOFTWARE: PATENTING DATE: 1995-12-18
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PATENTING VET. 2.0
SEQ ID NO 1
SEG ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
Conservative:
Mismatches:
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Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels:
                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Foot-and-mouth disease virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09091219 Patent No. 6171592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: equine rhinovirus 1
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TITLE OF INVENTION: A METHOD FOR EFFICIENT AND HIGHLY
TITLE OF INVENTION: SELECTIVE CONTROL OF MICROORGANISMS
FILE REFERENCE: 50078/008002
CURRENT APPLICATION NUMBER: US/09/293,549
CURRENT FILING DATE: 1999-04-16
EARLIER PELLOR DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 11
LENGTH: 1619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGly 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-Acetylglucosaminyltransferase V Proteins and Sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 80303

COMPUTER READABLE FORM:
MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-771-009-1 (1-17) x US-09-293-549-11 (1-1619)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3: Greenlee and Winner, P.C.
5370 Manhattan Circle, Suite 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAPLICATION NUMBER: US/08/276,968A FILING DATE: 19-JUL-1994
-CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/905,795
FILING DATE: 29-JUN-1992
PRIOR APPLICATION NUMBER: US 08/016,863
FILING DATE: 10-FEB-1993
APPLICATION UNMBER: US 08/016,863
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-276-968A-21/C

Sequence 21, Application US/08276968A

Patent No. 6015701

GENERAL INFORMATION:

APPLICANT: Pierce, James M.

APPLICANT: Shoreibah, Mohamed G.

APPLICANT: Fregien, Beverly,

APPLICANT: Fregien, Nevis L.

TITLE OF INVENTION: N-Acetylglucosam

TITLE OF INVENTION: Proteins and Seq
                  Sequence 11, Application US/09293549 Patent No. 6440409
                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Saccharomyces cerevisiae
US-09-293-549-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Ferber, Donna M. REGISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31.9
46.00
75.00%
56.25%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                        GENERAL INFORMATION:
APPLICANT: G. Todd Milne
APPLICANT: Gerald Fink
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 53/v man.
CITY: Boulder
STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alignment Scores:
US-09-293-549-11
                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match:
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δy

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Db 1523 AACTGGGATGCACTGGCTGTGGCTGGGGGGTACTAAACTCAAGCCCTGGACCA 1470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AsnPheAspLeuLeuLysLeuAlaGlyAspVal---GluSerAsnProGlyPro 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/08241943
Patent No. 5602321
GENERAL INFORMATION:
APPLICANT: John, Maliyakal E.
TITLE OF INVENTION: TRANSGENIC COTTON PLANTS
TITLE OF INVENTION: PRODUCING HETEROLOGOUS BIOPLASTIC;
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/241,943
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Nicholas J. Seay, Quarles & Brady
STREET: First Wisconsin Plaza, One South
STREET: Pinckney St.,
STREET: P.O. Box 2113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-771-009-1 (1-17) x US-08-276-968A-21 (1-1692)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Seay, Nicholas J.
REGISTRATION UNDBER: 27,386
REFERENCE/DOCKET NUMBER: 11-229-9076-8
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: us/07/980,521
FILING DATE: 20-NOV-1992
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 34-9
TELECOMMUNICATION INFORMATION:
TELEFHONE: (303)-499-8080
TELEFAX: (303)-499-8089
TELEFAX: (303)-499-8089
TELEFAX: 49617824
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 1692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (608) 251-2484
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                  42.50
72.22%
55.56%
47.22%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 2..1366
US-08-276-968A-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-241-943-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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O
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DESCRIPTION: Genomic DNA

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1258 TTCGACCTGCTGTTCTGGAACGCCGACCACCACCTGCCGGGGCCG 1305
                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 PheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/108,193 and 07/732,243

FILING DATE: 08/108,193 and 01/32,243

FILING DATE: 40 and 17, 1993 and July 19, 1991

ATTORNEY/AGENT INFORMATION:

NAME: 1an C. MCLEOd

REGISTRATION NUMBER: 00,931

REFERENCE/DOCKET NUMBER: MSU 4.1-222

TELEPHONE: (517) 347-4100

TELEPHONE: (517) 347-4100

TELEPHONE: (517) 347-4103

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

TANGTH. 2019 Base Pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Processes For Producing
TITLE OF INVENTION: Polyhydroxybutyrate and Related
TITLE OF INVENTION: Polyhydroxyalkanoates in the
TITLE OF INVENTION: Plastids of Higher Plants
                                                                                                                                                                                                                                                                                                            Conservative:
                                                                                                                                                                                                                                                                                                                               Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                              US-09-771-009-1 (1-17) x US-08-241-943-25 (1-1770)
                                                                                                                                                                                                                                                                    Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Acer
OPERATING SYSTEM: MS-DOS (version 3.3)
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Christopher R. Somerville, APPLICANT: Christiane Nawrath, APPLICANT: Yves Poirier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-254-357-3
; Sequence 3, Application US/08254357
; Patent No. 5610041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 2190 Commons Parkway
CITY: Okemos
STATE: Michigan
                   MOLECULE TYPE: genomic DNA
HYPOTHETICAE: NO
PUBLICATION INFORMATION:
AUTHORS: PEOPLES
AUTHORS: SINSKEY
JOURNAL: J. Biol. Chem.
VOLUME: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ian C. McLeod
                                                                                                                                                                                                                                                                  192
42.00
62.50%
56.25%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yves Poirier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acid
EDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 3
                                                                                                                                                            PAGES: 15298-15303
DATE: 1989
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: L
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48864
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                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                       US-08-241-943-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                Query Match:
DB:
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APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Schryvers, Robin E
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Xang, Yan-Ping
APPLICANT: Transferin Receptor Genes of Moraxella
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE: 43
CORRESPONDENCE: ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                         1507 TTCGACCTGCTGTTCTGGAACGCCACCACCAACCTGCCGGGGCC 1554
                                                                                                                                                                                                                                                                                                                                                  2 PheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/778,570B
FILING DATE: 03-JAN-1997
ATTORNEY APPLICATION: 536
                                                                                                                                                                                                           Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                          US-09-771-009-1 (1-17) x US-08-254-357-3 (1-2019)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                       Length:
Matches:
                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 1038-664 TELECOMMUNICATION INFORMATION:
                                        окGANISM: Alcaligenes eutrophus
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08778570B Patent No. 6437096 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPANE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 2127 base pairs
                                                                                                                                                                       225
42.00
62.50%
56.25%
46.67%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
42.00
84.62%
53.85%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                             Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
              ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: ALCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
HYPOTHETICAL:
                                                                                                                                                       Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-778-570B-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-778-570B-8
                                                                                                            US-08-254-357-3
                                                                                              LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                    Query Match:
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                                                                                                                                                                                             Score:
                                                                                                                                                                         Pred.
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TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: $1m & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
    00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                             391 GATGTTGTAAAACTTGAAGGTGACTTGAAGCATAATCCA 429
                                                                                                    3 AspLeuLeuLysLeuAlaGlyAspValGluSerAsnPro 15
                                                           US-09-771-009-1 (1-17) x US-08-778-570B-8 (1-2127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-771-009-1 (1-17) x US-09-059-584-8 (1-2127)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,570
FILING DATE: 03-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1038-794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,584
FILING DATE: 14-APR-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         Schryvers, Anthony B
Harkness, Robin E
Loosmore, Sheena M.
Du, Run-Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERNEC/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPRA: (416) 595-1155
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
LENGTH: 2127 base pairs
                                                                                                                                                                                                                          Sequence 8, Application US/09059584 Patent No. 6440701 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                       APPLICANT: Schryvers, Anthony APPLICANT: Harkness, Robin E APPLICANT: Loosmore, Sheena PAPLICANT: Du, Run-Pan APPLICANT: Yang, Yan-Ping APPLICANT: Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                          Myers, Lisa E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Toronto STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                     RESULT 11
US-09-059-584-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-059-584-8
                                                                                                                                                                                                                                                                                          APPLICANT
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score:
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391 GATGTTGTAAAACTTGAAGGTGACTTGAAGCATAATCCA 429

RESULT 12

3 AspLeuLeuLysLeuAlaGlyAspValGluSerAsnPro 15

δλ

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APPLICANT: Myers, Lisa E
APPLICANT: Schryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Harkness, Robin E
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
CORRESPONDENCE: 60
CORRESPONDENCE: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 GATGTTGTAAAACTTGAAGGTGACTTGAAGCATAATCCA 417
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                                                                                                                                                                                                                                                                                          E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/778,570 FILING DATE: 03-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/059,584 FILLING DATE: 14-APR-1998 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1038-794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7, Application US/08778570B
Patent No. 6437096
GENERAL INFORMATION:
APPLICANT: Myers, Lisa E
APPLICANT: Barryvers, Anthony B
APPLICANT: Harkness, Robin E
APPLICANT: Loosmore, Sheena M.
APPLICANT: Du, Run-Pan
APPLICANT: Yang, Yan-Ping
Sequence 50, Application US/09059584; Patent No. 6440701; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Stewart, Michael I
REGISTRATION NUMBER: 249738
REFERENCE/DOCKET NUMBER: 1038
RELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELERAX: (416) 595-1155
INFORMATION FOR SEQ ID NO: 50:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 2139 base pairs
                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                          ADDRESSEE:
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US-08-778-570B-7
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ADDRESSEE:
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US-09-059-584-7
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APPLICANT: Schryvers, Robin E
APPLICANT: Lossmore, Sheena M.
APPLICANT: Lossmore, Sheena M.
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & Manner
Streen
                        TITLE OF INVENTION: Transferrin Receptor Genes of Moraxella
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                    COMPUTE: CAUDAES:
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
21P: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: PatentIn Release #1.0, Version #1.30
COMPUTER: O3-JAN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 24973
REFERENCE/FOCKET NUMBER: 1038-664
TELCOMMUTCATION NUMBER: 1038-664
TELEFRANCE/FOCKET NUMBER: 1038-664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1083 GATGTTGTAAAACTTGAAGGTGACTTGAAGCATAATCCA 1121
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
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Indels:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT: Klein, Michel H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity:
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TOPOLOGY: lin
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RESULT 15
US-08-472-358-1
Sequence 1, Application US/08472358
Patent No. 5650555
GENERAL INFORMATION:
APPLICAMT: Chris Somerville, Yves Poirier,
APPLICANT: Douglas Dennis
TITLE OF INVENTION: Transgenic Plant Materials
TITLE OF INVENTION: Producing Polyhydroxyalkanoates
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Db 1083 GAIGTIGTAAAACTIGAAGGTGACTIGAAGCATAATCCA 1121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 AspLeuLeuLysLeuAlaGlyAspValGluSerAsnPro 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-771-009-1 (1-17) x US-09-059-584-7 (1-3435)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 48864
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 5.25 inch, 360 kb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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APPLICATION NUMBER: US/08/472,358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
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TELECOMMUNICATION INFORMATION:
                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/778,570
ELLING DATE: 03-JAN-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
                        омакк: US/09/059,584
14-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/732,243
FILING DATE: July 19, 1991
ATTONNEY/AGENT INFORMATION:
NAME: Ian C. McLeod
REGISTRATION NUMBER: 20,931
                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24973
REFERENCE/DOCKET NUMBER: 138
TELECOMMUNICATION INFORMATION:
TELEFRONE: (416) 595-1155
TELEFRAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3435 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Ian C. McLeod
STREET: 2190 Commons Parkway
CITY: Okemos
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84.62%
53.85%
46.67%
                   CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Okemos
STATE: Michigan
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Best Local Similarity:
Query Match:
                                                           FILING DATE: 1. CLASSIFICATION:
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Search completed: January 24, 2003, 20:17:40 Job time : 70 secs

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DNA encoding a fus
DNA encoding a fus
Plant dwarfing/stu
Human papillomavir

Sequence of part o Plant dwarfing/stu Retrovirus vector. Fragment from LITM Fragment from LITM

PRRSV attenuated v

Description

SUMMARIES

DB

Sequence encoding Foot and Mouth Dis Sequence encoding

AAN20016 ABL53056 AAN40073 AAN40074 AAN40075

AAT85178

Equine rhinovirus

Fragment from Fragment from

Sequence encoding Quorum sensing con

Sequence encoding

Drosophila melanog

ABL08841 ABL08079

ABL08840 ABL08078 ABA19679

AAF77900

Drosophila melanog

Drosophila melanog Drosophila melanog Human immune/haema

Human nervous syst

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Length
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                                                   Result
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-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
                                                                                                                                  January 24, 2003, 18:38:14; Search time 301 Seconds (without alignments) 127.189 Million cell updates/sec
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/SIDS2/gcgdata/geneseg/genesegn-embl/NA2002.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                          nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2185239 segs, 1125999159 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                    , Xgapext
, Ygapext
, Fgapext
, Delext
                                                                                                                                                                                                                                                                                NFDLLKLAGDVESNPGP 17
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                Xgapop 10.0,
Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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17:
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Perfect score:
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                                                                                             protein
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Human ORFX polynuc
DNA encoding novel
DNA sequence encod
DNA encoding novel
DNA encoding novel Aspergillus oryzae Arabidopsis thalia Eucalyptus grandis Human UGT1A7 relat Human UGT1A7 relat Human immune/haema Drosophila melanog Drosophila melanog P. putida KT2440-a Human immune/haema Drosophila melanog Streptococcus poly Orosophila melanog Genomic sequence PRRSV; Lelystad virus; pig viral infection; vaccine; attenuated virus; PRRSV attenuated virus vaccine PCR primer LV139(14609). Porcine reproductive and respiratory syndrome virus ALIGNMENTS AAS79520 AAZ30308 ABA9052 ABN26099 AAK78397 ABN6675( AAA99502 standard; DNA; 72 BP 15-FEB-2001 (first entry) 17245 31882 2365589 1767 19468 21399 654 1152 49380 WO200053787-A1 14-SEP-2000. Ray JA;

Evans IJ,

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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) I and the antifungal protein 2 (RSAF2), linked by a linker propertide of the invention. The specification describes methods for plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two basic or one acidic and one basic residue as a cleavable linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antimicrobial protein; AMP1; transgenic plant; linker propeptide; protein expression; plant defensin; RSAFP2; antifungal protein; AFP2; ss.
                                                                                                         Improving expression of polyproteins in plants involves coexpression of two or more proteins in plants within a single transcription unit \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "fusion protein of DmAMP1 and RSAFP2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 488 BP; 117 A; 116 C; 131 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA encoding a fusion protein of DmAMP1 and RSAFP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
                  De Bolle MFC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-771-009-1 (1-17) x AAZ99338 (1-488)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 3..566
                                                                                                                                                                Disclosure; Fig 33; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                  Broekaert WF, Francois IEJA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.79e-07
90.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ99339 standard; DNA; 575
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98GB-0026753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                   WPI; 2000-246564/21.
P-PSDB; AAY84071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dahlia merckii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200011175-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-AUG-1998;
04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          sedneuce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAZ99339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                                                                      The present sequence is one of the PCR primers used during the production of a vaccine against the porcine reproductive and respiratory syndrome virus (PRRSV, also known as Lelystad virus). This virus causes respiratory problems in pigs and abortions in sows. The N-protein can be mutated to produce an attenuated virus which acts as a vaccine in pigs against PRRSV. This has the advantage that it is highly immunogenic with less virulence than previous vaccines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antimicrobial protein; AMP1; transgenic plant; linker propeptide; protein expression; plant defensin; RsAFP2; antifungal protein; AFP2; ss.
                                                                                                                                                                                              Porcine reproductive and respiratory syndrome virus replicon useful a non-spreading and marker vaccine, has deletions of certain nucleic acid of original virus and is capable of in vivo RNA replication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /*tag= a
/product= "fusion protein of DmAMP1 and RsAFP2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA encoding a fusion protein of DmAMP1 and RSAFP2.
                                                                                      (DIEN-) STICHTING DIENST LANDBOUWKUNDIG ONDERZOE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 72 BP; 20 A; 22 C; 19 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative:
                                                                                                                            Langeveld J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers 3..479 /*tag= a
                                                                                                                                                                                                                                                                        Disclosure; Page 40; 52pp; English
                                                                                                                            Van Nieuwstadt AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.87e-08
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                 08-MAR-2000; 2000WO-NL00152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ99338 standard; DNA; 488
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                              WPI; 2000-594332/56.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dahlia merckii.
Unidentified.
                                                                                                                          Meulenberg J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200011175-A1
                                                   08-MAR-1999;
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04-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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Query Match:

AAZ99338

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The present sequence encodes a protein of the invention, comprising the mature proteins of the plant defensins, the Dahlia antimicrobial protein (AMP) I and the antifungal protein 2 (RSAFP2), linked by a linker propeptide of the invention. The specification describes methods for improving expression levels of one or more proteins in a transgenic plant. The method comprises inserting a DNA sequence having a promoter region operably linked to two or more protein encoding regions separated by a DNA sequence coding for a linker propeptide and a terminator region. The method is used to produce proteins in plants. The linker propeptide comprising a cleavage site, whereby the expressed polyprotein is post-translationally processed into the component protein molecules. The propeptide sequence is rich in amino acids A, V, S and T and contains dipeptidic sequences consisting of either two acidic, two
                                                                                                                                                                                                coexpression of
                                                                                                                                                                                          Improving expression of polyproteins in plants involves coexpressi
two or more proteins in plants within a single transcription unit
                                                         Ray JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ss; dwarfism; stunting; EST; expressed sequence tag;
                                                         De Bolle MFC, Evans IJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 575 BP; 133 A; 137 C; 149 G; 156 T; 0 other;
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Mismatches:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
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                                                                                                                                                                                                                                                                       Disclosure; Fig 34; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transgenic plant; plant metabolism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABK31150 standard; cDNA; 873 BP
                                                      Broekaert WF, Francois IEJA,
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20-JUL-2000; 2000US-219810P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-APR-2002 (first entry)
                                                                                                          2000-246564/21.
(ZENE ) ZENECA LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity:
Query Match:
                                                                                                                                      P-PSDB; AAY84072
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REDDY S A. LARRINUA M I. RUEGGER M. CHEM CO.

(LARR/) (RUEG/) REDD/)

(DOWC ) DOW

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The invention relates to polynucleotide and amino acid sequences
identified in one or more metabolic pathways that lead to dwarfism and
stunting in plants. Also included are vectors comprising the
copynucleotides, transgenic plants (including the seed and leaf)
transfected with the polynucleotides or vectors, a process for altering
the metabolism of a plant comprising providing the above vector and a
coplant, and transfecting the plant with the vector under conditions such
that the metabolism of the plant is altered by expression of the isolated
coplant, and plant is produced and a process for the characterisation of
that the metabolism of the plant is altered by expression of the isolated
coplant and blant is produced and a process for the characterisation of
tractionated biological samples, comprising (a) providing one or more
coplants, a mass spectroscopy apparatus or data analysis software and
coplants, a mass spectroscopy apparatus or data analysis software and
coplants, and the fractionated biological samples and the reference samples, the fractionated biological samples and
coplants with the gas coromatography apparatus to generate chromatographic
coplants amples, (c) treating the fractionated biological samples and
coplants and the reference samples with the mass spectroscopy apparatus to generate
coplants and the reference samples with the mass spectroscopy apparatus or generate
coplants and the reference samples and (d) processing the chromatographic and the
coplants and the reference samples and data analysis software. The nucleic caid and
the vector are useful for altering the metabolism of a plant and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant cDNA contig or singleton (related to dwarfism/stunting) identified by searching a nucleic acid database with plant EST (expressed sequence tag) and a BLAST (basic local alignment tool) stringency
                                                                                                                                                                                                                                                                                                                          Polynucleotide and amino acid sequences identified in one or more metabolic pathways that lead to dwarfism and stunning in plants, useful in agriculture to create dwarf varieties of any plant species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the vector are useful for altering the metabolism of a plant and for stunting a plant. The nucleic acids are useful in agriculture to create
                                                                                                                                                                                                                                               Pell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is a
                                                                                                                                                                                                                            Pogue PG;
Grosley R,
                                                                                                                                                                                                         Blakeslee B;
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                                                                                                                                                                                                    Ruegger M, Weglarz T, Bla
, McCrery AD, Miller AB,
MG, Zheng W, Gachotte D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
Indels:
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Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dwarf varieties of any plant species.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-771-009-1 (1-17) x ABK31150 (1-873)
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 9; 717pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAD35101 standard; DNA; 939 BP
                                                                                                                                                                                                                        Oriedo VBJ, Savickas JP, M
Della-Cioppa RG, Wolfe MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.58e-07
90.00
100.00%
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                                                                                                                                                                                                         Larrinua MI,
                 BLAKESLEE B.
ORIEDO V B J.
SAVICKAS J P.
                                                                               MCCRERY A D.
                                                                                                MILLER A B.
GACHOTTE D.
GROSLEY R.
                                                                                                                                                                                                                                                                                      WPI; 2002-164823/21.
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Query Match:
                                                                                                                                                                (PELL/) PELL R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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                                                           (SAVI/)
(MCCR/)
                                                                                                                     (GACH/)
(GROS/)
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                   (BLAK/)
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Dp
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Keller

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The inventors claim DNA sequences that encode antigenic polypeptides of FMDV selected from FMDV-715, FMDV-144, FMDV-1034, FMDV-1448, FMDV-1824, FMDV-1933, VPI-1, VPI-5 FMDV-1034-Bal or FMDV-1034-Bal (ECORI-HindIII). In particlar, FMDV serotypes O, A, C, SAT 1, SAT 2, SAT 3, and Asian type I. FMDV antigenic polypeptides are also claimed.
                                                                                                                                                                                                                                                                                                                          Polypeptide(s) with foot and mouth disease antigen specificity produced from DNA sequences by transformed hosts etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant; ss; dwarfism; stunting; EST; expressed sequence tag; transgenic plant; plant metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 961 BP; 251 A; 278 C; 240 G; 192 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches:
Indels:
                                                                                                                                                                                                                                              Schaller H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-771-009-1 (1-17) x AAN10025 (1-961)
                                                                                                                                                                                                                                                                                                                                                                         Example; Fig 9-10; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK31034 standard; cDNA; 1105 BP
   /product= VP1
701..961
                                                                                                                                                                                                                                            Nofschneider PH, Kupper HA,
                                                                                                                                81EP-0302080
                                                                                                                                                               80GB-0026661
                                                                                                                                                                              80GB-0015635
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2000US-219810P.
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                                  /*tag=
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                                                                                                                                                                                                              (BIOG-) BIOGEN NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                           P-PSDB; AAP10034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200208410-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-JUL-2000;
20-JUL-2000;
                                                                                                                                11-MAY-1981;
                                                                                                                                                               15-AUG-1980;
                                                                                                                                                                                12-MAY-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                02-DEC-1981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2002
                                                                EP40922-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABK31034;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Planta.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABK31034/c
                  CDS
    δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to an alphavirus vector system comprising nucleic acid derived from a human papilloma virus (HPV). The invention or cells containing it, are used in treatment and prevention of cervical cancer, particularly as a vaccine. By selecting the nucleic acid that encode E6/F7 proteins without ability to bind to pRb and p53, the risk that cells infected with the alphavirus vector system may become oncogenic is avoided (contrast use of other viral vectors). The present sequence is Human papillomavirus enhE6,7 constrcut DNA.
                                                                                                                                                                                                                                                                                                                                                                      New alphavirus system, useful for genetic immunization against cervical cancer, comprises papilloma virus nucleic acid -
                                                             Alphavirus vector system; human papilloma virus; HPV; cervical cancer; therapy; vaccine; virucide; cytostatic; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of part of the sequence of DNA insert FMDV-1034 including the structural gene for \ensuremath{\mathrm{VPl}}\xspace .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           939
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                                                                                                                                                                                                                                                                                                          Daemen CAHH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vaccine; foot and mouth disease; antigen; ss
                                 Human papillomavirus enhE6,7 constrcut DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
Matches:
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Gaps:
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                                                                                                                                                                                                                                                                                                          Holtrop M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 19; 45pp; English.
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90.00
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                                                                                                                                                                                                            06-OCT-2000; 2000EP-0203472
                                                                                                                                                                                                                                          06-OCT-2000; 2000EP-0203472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAN10025
ID AAN10025 standard; DNA; 961
                                                                                                                                                                                                                                                                          (UYGR-) RIJKSUNIV GRONINGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
25-JUL-2002 (first entry)
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/*tag=
62..700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag=
                                                                                                            Human papillomavirus
                                                                                                                                                                                                                                                                                                                                      WPI; 2002-354156/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                           EP1195438-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-AUG-1992
                                                                                                                                                                             10-APR-2002
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Query Match:

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CDS

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(RIGE-) RIGEL PHARM INC.
    The involution ligitation to purply uncontrol and and according to perfect the feature of the involution ligitation of more metabolic pathways that lead to dwarfism and stunting in plants. Also included are vectors comprising the seed and leaf) transfected with the polynuclectides or vectors, a process for altering the plant comprising providing the above vector and a plant, and transfecting the plant with the vector under conditions such that the metabolism of the plant is altered by expression of the isolated nucleic acid from the vector, e.g. such that a stunting phenotype in an industrial plant is produced and a process for the characterisation of fractionated biological samples, references samples, a gas chromatography of fractionated biological samples, references samples, and the reference corresponding to the fractionated biological samples and the reference samples with the gas chromatography apparatus to generate chromatographic at a corresponding to the fractionated biological samples and the reference samples with the mass spectroscopy apparatus to generate chromatographic corresponding to the fractionated biological samples and the reference samples with the mass spectroscopy apparatus to generate chromatographic corresponding to the fractionated biological samples and the reference samples with the data analysis software. The nucleic acid and the reference samples and (4) processing the chromatographic and the reference samples and (4) processing the chromatographic acid and the reference samples and (4) processing the chromatographic acid and corresponding to the fractionated biological samples containing a plant. The nucleic acids are useful in agriculture to create dwarf varieties of any plant species. The present sequence is a companion of the rearching a plant species. The present sequence is a companion of the rearching a plant species. The present sequence is a companion of the rearching a plant species. The present sequence is a companion of the rearching a plant species. The present seque
                                                                                                                                                                                                                                                                                                                                                                                                                           Polynucleotide and amino acid sequences identified in one or more metabolic pathways that lead to dwarfism and stunning in plants, useful in agriculture to create dwarf varieties of any plant species -
                                                                                                                                                                                                                                                                                                                                         Pell R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by searching a nucleic acid database with plant EST (expressed sequence tag) and a BLAST (basic local alignment tool) stringency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to polynucleotide and amino acid sequences
                                                                                                                                                                                                                                                                                          Reddy SA, Larrinua MI, Ruegger M, Weglarz T, Blakeslee B;
Oriedo VBJ, Savickas JP, McCrery AD, Miller AB, Pogue PG;
Della-Cioppa RG, Wolfe MG, Zheng W, Gachotte D, Grosley R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1105 BP; 308 A; 265 C; 262 G; 270 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 9; 717pp; English.
REDDY S A.
LARRINUA M I.
RUEGGER M.
WEGLARZ T.
                                                                                      BLAKESLEE B.
ORIEDO V B J.
SAVICKAS J P.
MCCRERY A D.
                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-164823/21
                                                                                                                                                                             MILLER A B. GACHOTTE D.
                                                                                                                                                                                                                           GROSLEY R.
                                                                                                                                                                                                                                                   PELL R.
                                                               (WEGL/)
(BLAK/)
(ORIE/)
(SAVI/)
(MCCR/)
(MILL/)
(GACH/)
(GROS/)
                                                                                                                                                                                                                                                (PELL/)
                                              RUEG/
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17 0 0 0 Conservative: Mismatches: Length: Matches: Indels: 1.27e-06 90.00 100.00% 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: Query Match: 

US-09-771-009-1 (1-17) x ABK31034 (1-1105)

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AAZ34936 ID AAZ3 RESULT 8

AA234936 standard; DNA; 5715 BP

Interleukin-4 inducible epsilon promoter; IgE; immunoglobulin; antibody; modulator; screening; human; allergy; therapy; retrovirus; vector; green fluorescent protein; GFP; ss. /note= "pGEM backbone (pUC origin, ampR)" "green fluorescent protein" /*tag= d /note= "FMDV 2a cleavage sequence" 1..845
/*tag= a
/note= "CMV promoter/R/U5 5' LTR" /*tag= b /note= "GAG ATG-ATC mutation" Location/Qualifiers LTR" replace(1322,G) Chimeric - cytomegalovirus. Chimeric - Aequoria victoria. Chimeric - unidentified. /product= "c 2895..2952 /*tag= e /note= "3' 3652..5715 2151..2865 .3645 (first entry) O /*tag= /*tag= Retrovirus vector. 28-FEB-2000 misc_feature misc_feature AAZ34936; mutation promoter CDS LTR

WO9958663-A1 18-NOV-1999

99WO-US10497 98US-0076624 12-MAY-1999; 12-MAY-1998; Armstrong R, Swift SE, DA, Ferrick

В; Fox

WPI; 2000-062297/05.

Methods, cell lines and vectors for screening for modulators of immunoglobulin E synthesis, secretion and switch rearrangement

Disclosure; Fig 11B; 81pp; English.

This is the nucleotide sequence of a retrovirus vector preferred for use in methods of the invention. The invention provides methods of screening for bloactive agents capable of inhibiting the human interleukin-4 (ILI-4) inducible epsilon promoter (see AA234932). The method comprises combining a candidate bloactive agent with a cell comprising a fusion nucleic acid composed of the IL-4 inducible epsilon promoter and a reporter gene. The promoter is then induced with IL-4 or IL-13, and the presence or absence of the reporter comprises comprises that the presence of the reporter pene indicates that the agent inhibits the promoter. Preferred embodiments use retroviral vectors to introduce the candidate bloactive agents. Also provided control in the complexity of screening for bloactive agents capable of modulating IE synthesis, secretion and switch rearrangment. These methods inducible epsilon promoter that starts a cascade that IL-4 inducible epsilon promoter that starts a cascade that ultimately inducible is inducible epsilon promoter that starts a cascade that ultimately results in IgE production. The methods screen for upstream modulators of IgE production to prevent the production of IgE and thus reduce or eliminate the allergic response.

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production, by using diphtheria toxin constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                         AAT92989;
                                                                                                                                                                                                                                                                    Query Match:
                                                                                                                                                                                                                                                                                                                                                     RESULT
Screening for agents capable of inhibiting a promoter, especially interleukin-4 inducible epsilon promoter involved in immunoglobulin E
                                                                                                                                                                                                                                        Interleukin-4 inducible epsilon promoter; human; IgE; antibody;
immunoglobulin E; allergy; therapy; switch rearrangement; vector;
CMV; green fluorescent protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                    "green fluorescent protein fusion with
C-terminal GGGSGGG linker and FMDV 2a
cleavage sequence"
                                                                                                                   2904 AATTTTGACCTTCTTAAACTTGCGGGGGAGACGTCGAGTCCAACCCTGGGCCC 2954
                                                                                                           1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
Sequence 5715 BP; 1342 A; 1610 C; 1419 G; 1344 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= g
/note= "pGEM backbone (pUC origin, ampR)"
                         5715
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                        Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                        'note= "extended psi region"
151..2865
                                                                       Gaps:
                                                                                        US-09-771-009-1 (1-17) x AAZ34936 (1-5715)
                                                                                                                                                                                                                                                                                                                                                    /*tag= b
/note= "CMV promoter"
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..845
/*tag= a
/note= "5' LTR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= f
/note= "3' LTR"
3652..5715
                                                                                                                                                                                                                                                                                                                        a
."5' LTR"
                                                                                                                                                                AAF30945 standard; DNA; 5715 BP
                                                                                                                                                                                                                                                                                                                                                                      replace(1322,G)
                        9.03e-06
90.00
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    Cytomegalovirus.
    Unspecified.

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850..2100
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-
                                                                                                                                                                                                                       Vector used in invention.
                                                                                                                                                                                                                                                                                                                                           1..845
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                 '*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (RIGE-) RIGEL PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                            /*tag=
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                                            Percent Similarity:
Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                        misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1999;
                  Alignment Scores:
                                                                                                                                                                                                    23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kinsella TM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-MAY-2001
                                                                                                                                                                                                                                                                             Chimeric
Chimeric
                                                                                                                                                                                  AAF30945;
                                                                                                                                                                                                                                                                                                                                                                       mutation
                                                                                                                                                                                                                                                                                                                                            promoter
                                                               Query Match:
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                                                                                                                             g
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The present sequence is that of a vector preferred for use in methods of the invention. These methods utilise diphtheria toxin for screening purposes, especially for identifying modulators of 195 synthesis, secretion and switch rearrangement. A claimed method of screening for bloadtive agents capable of inhibiting the 200 method of screening for bloadtive agents capable of inhibiting the 200 method of screening for bloadtive agents and a cell that does not endogenously express heparin-binding epidermal growth factor-like growth factor (HBEGF) and which comprises a claison nucleic acid encoding HBEGF; inducing the promoter with IL-4; adding diphtheria toxin to the cell; and determining whether the cell is dead. Compositions comprising a test vector and a reporter vector that includes a reporter gene such as green fluorescent claiming a provided. Inhibitors of IgE synthesis can be identified that prevent the production of IgE and reduce or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virus like particle, diagnostic reagent, antibiotic, therapy; VLP; food supplement; vaccination; herbicide resistance; industrial enzyme; tobacco mild green mosaic virus; TMGMV; PCR primer; LITMUS 39; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Production of virus like particles – using a nucleic acid sequence capable of assembly with a protein having a first viral portion and second non-viral portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 5715 BP; 1342 A; 1610 C; 1419 G; 1344 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fragment from LITMUS 39 based plasmid pLit.GFP-2A16H-CP.
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Indels:
Disclosure; Fig 11B-1-11B-3; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-771-009-1 (1-17) x AAF30945 (1-5715)
                                                                                                                                                                                                                                                                                                                                                              eliminate an allergic response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCCR-) SCOTTISH CROP RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.03e-06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chapman SN, Wilson TMA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1997-526468/48.
P-PSDB; AAW33911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Potato virus X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9739134-A1
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This is a fragment from the LITMUS 39 based plasmid pLit.GFP-2A16H-CP.
These plasmids contain the green fluorescent protein (GFP)-2A- potato virus X coat protein (CP) gene fusions. This is used as a source for GFP-2A gene fusion with tobacco mild green mosaic virus (TMGMV) coat protein (CP) gene and 3' UTR. This is used in a novel method for producing a protein having a first (viral) portion and a second (non-viral) portion. The method comprises, expressing the protein in a cell, providing a nucleic acid sequence capable of assembly with the protein into a virus-like particle (VLP), and permitting in vivo assembly of the protein and nucleic acid into VLPs. The VLPs can be used for the production of proteins and adaptostic reagents, antibiotics,
                                                                                                                                                                                                                                                                                                                                                                                                                        therapeutic agents or food supplements. They can be used for e.g. expression of metabolic enzymes for pathway engineering, nutritional supplements, anti-potato cyst nematode lectins, gut protease inhibitors, anti-botrytis agents, pGIPs, anti-insect Bacillus thuringiensis toxin and herbicide resistance agents, industrial enzymes, pharmaceuticals, therapeutic proteins, and nucleic acids, and as bioreactors. They can also be used intact for presentation of peptide epitopes for vaccination of animals, the production of therapeutic or industrial proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     polypeptides and/or the delivery of therapeutic nucleic acid molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 60 BP; 13 A; 15 C; 16 G; 16 T; 0 other;
                             Example 2; Fig 4; 33pp; English.
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00000 Conservative: Mismatches: Matches: Length: Indels: Gaps: 7.16e-07 83.00 100.00% 92.22% Similarity: Percent Similarity: Alignment Scores: Query Match: Best Local Score: Pred.

US-09-771-009-1 (1-17) x AAT92989 (1-60)

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Fragment from LITMUS 39 based plasmid pLit.GFP-2A16K-CP. AAT92990 standard; DNA; 60 BP 24-APR-1998 (first entry) AAT92990; RESULT 11 AAT92990 

Virus like particle; diagnostic reagent; antibiotic; therapy; VLP; food supplement; vaccination; herbicide resistance; industrial enzyme; tobacco mild green mosaic virus; TMGMV; PCR primer; LITMUS 39; ss.

Potato virus X. Synthetic

WO9739134-A1.

97WO-GB01065 17-APR-1997; 23-OCT-1997

96GB-0007899 17-APR-1996; (SCCR-) SCOTTISH CROP RES INST.

Chapman SN, Wilson TMA;

WPI; 1997-526468/48. P-PSDB; AAW33911 Production of virus like particles - using a nucleic acid sequence

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This is a fragment from the LITMUS 39 based plasmid plit.GPP-2A16K-CP.
These plasmids contain the green fluorescent protein (GFP)-2A- potato
virus X coat protein (CP) gene fusions. This is used as a source for
GFP-2A gene fusion with tobacco mild green mosaic virus (TMGMV) coat
protein (CP) gene and 3' UTR. This is used in a novel method for
producing a protein having a first (viral) portion and a second
(non-viral) portion. The method comprises, expressing the protein in a
cell, providing a nucleic acid sequence capable of assembly with the
protein into a virus-like particle (VLP), and permitting in vivo assembly
of the protein and nucleic acid into VLPs. The VLPs can be used for the
production of proteins such as adiagnostic reagents, antibiotics,
therapeutic agents or food supplements. They can be used for e.g.
expression of metabolic enzymes for pathway engineering, nutritional
                                                                                                                                                                                                                                                                                                                                                                                                                                   supplements, anti-potato cyst nematode lectins, gut protease inhibitors, anti-borytis agents, pGIPs, anti-insect Bacillus thuringtensis toxin and herbicide resistance agents, industrial enzymes, pharmaceuticals, therapeutic proteins, and nucleic acids, and as bioreactors. They can also be used intext for presentation of peptide epitopes for vaccination of animals, the production of therapeutic cor industrial proteins and polypeptides and/or the delivery of therapeutic nucleic acid molecules.
capable of assembly with a protein having a first viral portion and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 60 BP; 13 A; 15 C; 17 G; 15 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                    Example 2; Fig 4; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7.16e-07
83.00
100.00%
100.00%
92.22%
                         second non-viral portion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Alignment Scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score:
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Indels: US-09-771-009-1 (1-17) x AAT92990 (1-60) Query Match: g

BP. AAT92988 standard; DNA; 81 AAT92988; RESULT 12

24-APR-1998 (first entry)

Virus like particle, diagnostic reagent, antibiotic, therapy, VLP; food supplement, vaccination, herbicide resistance, industrial enzyme; tobacco mild green mosaic virus; TMGMV; PCR primer; LITMUS 39; ss. Fragment from LITMUS 39 based plasmid pLit.GFP-2A23H-CP. 97WO-GB01065 Potato virus X. WO9739134-A1. 17-APR-1997; 23-OCT-1997. Synthetic 

(SCCR-) SCOTTISH CROP RES INST. 96GB-0007899. Chapman SN, Wilson TMA; 17-APR-1996;

WPI; 1997-526468/48 P-PSDB; AAW33910

```
These plasmids contain the green fluorescent protein (GFP)-2A-potato virus X coat protein (CP) gene fusions. This is used as a source for the green fluorescent protein (GFP)-2A-potato virus X coat protein (CP) gene fusions. This is used as a source for gene and 3' UTR. This is used in a novel method for protein (CP) gene and 3' UTR. This is used in a novel method for contain the protein having a first (viral) portion and a second (con-viral) portion. The method comprises, expressing the protein in a cell, providing a nucleic acid sequence capable of assembly with the protein into a virus-like particle (VLP), and permitting in vivo assembly of the protein and nucleic acid sequence capable of assembly with the protein and nucleic acid into VLPs. The VLPs can be used for the protein and nucleic acid supplements. Anti-picies, anti-picies, charapeutic agents or food supplements. They can be used for e.g. expression of metabolic enzymes for pathway engineering, nutritional capable of metabolic enzymes for pathway engineering, nutritional anti-botrytis agents, pidistrial enzymes, pharmaceuticals, canti-botrytis agents, industrial enzymes, pharmaceuticals, contens, and nucleic acids, and as bioreactors. They can also be used intact for presentation of peptide epitopes for vaccination of animals, the production of therapeutic or industrial proteins and contens and propeptides and/or the delivery of therapeutic nucleic acid molecules.
                                                                                                                                                                                                                           a fragment from the LITMUS 39 based plasmid pLit.GFP-2A23H-CP
                              Production of virus like particles - using a nucleic acid sequence capable of assembly with a protein having a first viral portion and
                                                                                                                                                              Example 2; Fig 4; 33pp; English.
                                                                                                  second non-viral portion
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Sequence 81 BP; 18 A; 20 C; 22 G; 21 T; 0 other;

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81
16
0
0
0
        Length:
Matches:
Conservative:
Mismatches:
                                         Indels:
                                                  Gaps:
       1.02e-06
83.00
100.00%
100.00%
92.22%
                       Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                         Query Match:
        Pred.
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US-09-771-009-1 (1-17) x AAT92988 (1-81)

δ g

AAT92991 standard; DNA; 183 BP 24-APR-1998 (first entry) AAT92991; RESULT 13 AAT92991 £ 

Fragment from LITMUS 39 based plasmid pLit.GFP-2A58K-CP.

Virus like particle; diagnostic reagent; antibiotic; therapy; VLP; food supplement; vaccination; herbicide resistance; industrial enzyme; tobacco mild green mosaic virus; TMGMV; PCR primer; LITMUS 39; ss.

Potato virus X. Synthetic.

WO9739134-A1.

23-OCT-1997

97WO-GB01065 96GB-0007899 17-APR-1997; 17-APR-1996;

(SCCR-) SCOTTISH CROP RES INST.

Chapman SN, Wilson TMA;

```
This is a fragment from the LITMUS 39 based plasmid pLit.GFP-2A58K-CP.
These plasmids contain the green fluorescent protein (GFP)-2A- potato
virus X coat protein (CP) gene fusions. This is used as a source for
GFP-2A gene fusion with tobacco mild green mosalc virus (TMGMV) coat
protein (CP) gene and 3' UTR. This is used in a novel method for
C protein (CP) gene and 3' UTR. This is used in a novel method for
C coll. portion. The method comprises, expressing the protein in a
C (non-viral) portion. The method comprises, expressing the protein in a
C cell, providing a nucleic acid sequence capable of assembly with the
CC protein into a virus-like particle (VLP), and permitting in vivo assembly
CC of the protein and nucleic acid into VLPs. The VLPs can be used for the
CC production of proteins such as diagnostic reagents, antibiotics,
C expression of metabolic enzymes for pathway engineering, nutritional
CC supplements, anti-potato cyst nematode lectins, gut protease inhibitors,
anti-borrytis agents, industrial enzymes, pharmaceuticals,
C herapeutic proteins, and nucleic acids, and as bioreactors. They can
also be used intact for presentation of peptide epitopes for vaccination
C animals, the production of therapeutic or industrial proteins and
C polypeptides and/or the delivery of therapeutic nucleic acid molecules.
                                                                             of virus like particles - using a nucleic acid sequence assembly with a protein having a first viral portion and
                                                                                                                                                                                         Example 2; Fig 4; 33pp; English.
                                                                                                                                     second non-viral portion
WPI; 1997-526468/48.
P-PSDB; AAW33912.
                                                                                Production capable of
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Sequence 183 BP; 51 A; 48 C; 47 G; 37 T; 0 other;

Alignment Scores:

.. No

1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGly 16 183 00 00 0 Length:
Matches:
Conservative:
Mismatches: Indels: Gaps: US-09-771-009-1 (1-17) x AAT92991 (1-183) 2.71e-06 83.00 100.00% 100.00% 92.22% Best Local Similarity: Percent Similarity: Query Match: DB: ò

1.

136 AATTTTGACCTTCTCAAGTTGCCGGAGACGTCGAGTCCAACCCTGGG 183 BP AAT85178 standard; DNA; 7277 AAT85178; RESULT 14 AAT85178 g

(first entry)

11-FEB-1998

Equine rhinovirus 1; ERhV1; foot-and-mouth disease virus; vaccine; horse; diagnosis; antigen; polyprotein; enzyme-linked immunosorbent assay; recombinant protein; ss. Equine rhinovirus 1 (ERhV1) polyprotein encoding nucleotide sequence. Equine rhinovirus 1. 

/*tag= b
/note= "polypyrimidine tract" /*tag= a /codon_start= putative Location/Qualifiers /*tag= c 7179..7277 /*tag= d 435..7178 misc_feature 5'UTR 3'UTR Key

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Foot and mouth disease virus
                       Key
                                                                       CDS
                                                                                                                     CDS
                                                                                                                                                                   CDS
                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                  CDS
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 The present sequence represents the nucleic acid sequence encoding the polyprotein (AAW27126) of equine rhinovirus 1 (ERNVI). The taxonomic status of ERNVI is unclear, as physicochemical studies have shown that the nucleic acid density and base comparison of ERNVI differs from other rhinoviruses. To this end, the nucleotide sequence encoding the collyprotein of ERNVI was deduced. Analysis of this sequence suggests that ERNVI is more closely related to foot-and-mouth disease virus. Comparison of ERNVI mas deduced. Analysis of this sequence suggests that ERNVI proteins can be used to foot-and-mouth disease virus. Composes can be used for diagnosis of ERNVI or related viruses, while antibodies in the blood particularly in enzyme-linked immunosorbent assay. They can differentiate between infected animals will have antibodies reactive with non-capsid proteins but vaccinated animals will not).

Comparison of the present sequence represent individual genes of the virus and can be expressed in host systems to produce recombinant proteins. Wirns like particles containing the individual ERNVI proteins, can also the useful agents, containing the individual ERNVI proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ncluding vaccinating epitopes from other pathogens or reproductive
                                                                                                                                                                                        Genomic sequence of equine rhinovirus 1 - and derived proteins or virus-like particles, useful in vaccines and as diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoding p20, VP4, VP2, VP3, VP1 and p52 in recombinant plasmid pFA A61/t 76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7277 BP; 1805 A; 1662 C; 1750 G; 2060 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine; antibody; capsid protein; immunogen; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
Matches:
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                                                                                                                                                                                      Genomic sequence of equine rhinovirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-771-009-1 (1-17) x AAT85178 (1-7277)
                                                                                                                                                                                                                           Claim 1; Pages 27-29; 60pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAN20016 standard; cDNA; 2802 BP
                                                                                                                               Crabb BS, Feng L, Studdert MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.000505
81.00
94.12%
88.24%
90.00%
                                                         96WO-AU00815.
                                                                               95AU-0007201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         foot and mouth disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                       (UYME ) UNIV MELBOURNE.
                                                                                                                                                     WPI; 1997-341692/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                  P-PSDB; AAW27126
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         WO9722701-A1
                                                         18-DEC-1996;
                                                                               18-DEC-1995;
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                                 26-JUN-1997
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The inventors claim a DNA molecule comprising a nucleotide sequence corresp. to all or a portion of foot-and-mouth disease virus RNA (FMDV). The DNA molecule is esp. for a precursor of FMDV capsid protein. It esp. codes for FMDV protein D88 and VPI-VP4. It may code for VP4, VP2, VP3 and VPI contiguously. The inventors also claim a vaccine for stiumlating prodn. of antibodies against FMDV in a mammal which comprises at least one of the above recombinant produced by a host cell transformed with the DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA corresp. to (part of) foot and mouth disease virus RNA - useful in prepn. of vaccines for producing antibodies against the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rowlands DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ASnPheAspLeuLeuLySLeuAlaGlyAspValGluSerAsnProGlyPro 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JC, Cross GAM, Highfield PE, Winther MD,
Harris TJR, Lowe PA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2802 BP; 714 A; 810 C; 689 G; 588 T; 0 other;
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Matches:
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Jocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 13; 57pp; English.
                                                                                                                                                                                                                                                                                                      /note= "claim 17"
1835..2470
                                                                                                                                                                                                                                                                                                                                                                                     /note= "claim 15"
2471..2802
                                                                                                                                                                                                                        /note= "claim 16"
1172..1834
                                                                                                                                           "claim 18"
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                                      /*tag= a
/product= p20
                                                                                                                                                                                                                                                                   /*tag= d
/product= VP3
                                                                                                                                                                                                       /product= VP2
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/product= VP4
                                                                                                                                                                                                                                                                                                                                                                    /product= VP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= p52
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80.00
94.128
98.128
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80GB-0034130
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81GB-0011064
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08-APR-1981;
18-AUG-1981;
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22-OCT-1980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EP48455-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown F,
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DB:
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X88855 Foot and mo
X88856 Foot and mo
X88857 Foot and mo
X88862 Foot and mo
X88869 Foot and mo
X88863 Foot and mo
X88861 Foot and mo
AR36450 Foot and mo
AR36457 Sequence
AX460903 Sequence
AX460903 Sequence
AX460903 Sequence
AX460903 Sequence
AX460903 Foot and mo
E00030 DNA coding
AX36441 Sequence
AX36441 Sequence
AX660030 DNA coding
AX36441 Foot and mo
X00130 Foot and mo
X01130 Foot and mo
X01130 Foot and mo
X151476 Foot and mo
AX146811 Sequence
AF0526168 Foot-and-AX151473 Foot and mo
X16812 Foot and mo
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AJ133359 Foot-and-
AJ133357 Foot-and-
AJ33857 Foot-and-
AF511039 Foot-and-
AJ007347 Foot-and-
AJ007347 Foot-and-
AJ20488 Foot-and-
AF506822 Foot-and-
AF506822 Foot-and-
AF51253 Equine rh
AF361253 Equine rh
AF167307 Foot-and-
AF167307 Foot-and-
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                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                            Description
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                                                                                                                                                                                                          SUMMARIES
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AX146811
AF026168
AF154271
FDI251473
PIFMDV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FMV7572
FDI320488
AF506822
                                                                                                                                                                                                                                                                FMDVAICP1
FMDVAICP2
FMDVAICP3
FMDV0CP02
                                                                                                                                                                                                                                                                                                                                    FMDVAICP4
FMDVOCP01
FMDVOCP03
AF024509
APHOVPIN
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AF274010
FAN133358
FAN133359
FD1133357
AF308157
AF511039
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FMDVA22CP
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AF167307
AF377945
AB079061
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AX403959
AX460903
A00276
E00030
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PIFMDV
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                      em_htg_inv:*
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             em_htg_hum:*
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Match Length
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3119
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94.4
92.2
92.2
330...
331...
332...
335...
336...
40...
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                                                                                                                                                                                                                                           Score
                                                                                                                                                                                                                                                                   RESULT 1
                                                                                                                                                                                                                                           No.
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                                                                                                                                                                                                                                                                                                                                                                 Command line parameters:
-MODEL-frame+_p2n.model.-DEV=Xlp
-QO=Cggn2_1/GSPTO_spool/US09771009/runat_22012003_140100_18450/app_query.fasta_1.199
-Q=/Cggn2_1/USPTO_spool/US09771009/runat_22012003_140100_18450/app_query.fasta_1.199
-Q=/Cggn2_1/USPTO_spool/US09771009/runat_22012003_1-COPCL=0.-LOOPEXT=0
-UNITS=b1ts.SCREN=T=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-UNITS=b1ts.SCREN=CTTR=T=1 - MATRIX=b100 -TRR_MIN=10 -ALIGEN=15 -MODE-LOCAL
-USTEN=US09771009_CGGN_1_1 3637_G*unat_22012003_140100_18450 -NCPU=6 -ICPU=3
-NO_XLDXY -NO_MANP -LARGEOURY -NGG_SCORES=0 -WAIT -LONGLOG -DEV_TMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPPOP=10 -XGAPPXT=0.5 -FGAPPOP=6 -FGAPPXT=7
                                                                          2003, 18:39:14 ; Search time 3166 Seconds (without alignments) 156.269 Million cell updates/sec
          GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                       nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                              of hits satisfying chosen parameters:
                                                                                                                                                                                                                                        2054640 seqs, 14551402878 residues
                                                                                                                                                                                                                                                                                                                                               Listing first 45 summaries
                                                                                                                                                                               Xgapop/10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                               NFDLLKLACDVESNPGP 17
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Maximum Match 100%
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Maximum DB seq length: 200000000
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9b_pr:*
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                                                                            January 24,
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Perfect score:
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                                                       OM protein
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FMDVAICP3 327 bp mRNA linear VRL 31-AUG-1995 Foot and mouth disease virus Asia I mRNA for capsid protein (partial) and protease (Nilgiri).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="SPTREMBL:067451"
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AVKAENITELLIRMKRAETYCPRPLLALDTTQDRRKQEIIAPEKQVLNFDLLKLAGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X88857.1 GT:971409
Za protease; 2B protease; immunogenic protein; polyprotein; VPI
gene; VPI protein.
Foot-and-mouth disease virus.
I i lases: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Aphthovirus.
I (bases: 1 to 327)
Tulasiram, P., Tyaqi, M. and Suryanarayana, V.
Antigenic variation in foot and mouth disease virus type Asia I
                                                                                   1 (bases 1 to 327)
Tulasiram,P., Tyagi,M. and Suryanarayana,V.
Antigenic variation in foot and mouth disease virus type Asia I
                                                                                                                                                                                                           Direct Submission
Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary
Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                                                                                                                                                                                             /product="immunogenic polyprotein with 2A protease"
/protein_id="CAA61326.1"
/db_xreff="G1:971408"
                                                  no DNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Foot-and-mouth disease virus"
/isolate="Asia I Mandya, Karnataka"
/db_xref="taxon:12110"
/map="3337-3669 of 1D with 2A of FMDV"
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117
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                  Foot-and-mouth disease virus.
Frot-and-mouth disease virus
Viruses; ssRNA positive strand viruses,
Picornaviridae; Aphthovirus.
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274. .321
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/product="2A protease"
322. .>377
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/product="2B
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/gene="VP1"
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                                                                                                                                                                                            Suryanarayana, V.V.S.
                                                                                                                                                                          (bases 1 to 327)
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 gene; VP1 protein.
                                                                                                                                         isolates of India
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                                                                                                                                                        Unpublished
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TITLE
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KEYWORDS
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         FMDVAICP1 327 bp mRNA linear VRL 31-AUG-1995 Foot and mouth disease virus Asia I mRNA for capsid protein (partial) and protease (Nainital).
                                                           X88855.1 GI:971405

X88855.1 GI:971405

Za protease; 2B protease; immunogenic protein; polyprotein; VP1

gene; VP1 protein.

Foot-and-mouth disease virus.

SM Foot-and-mouth disease virus.

Viruses; ssRNA positive-strand viruses, no DNA stage;

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Aphthovirus.

E 1 (bases 1 to 327)

Tulasiram,P., Tyagi,M. and Suryanarayana,V.

Antigenic variation in foot and mouth disease virus type Asia I isolates of India

L Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="APHRVLATVYNGKTTYGTQPTRRGDLAVLAQRVSNRLPTSFNYG
AVKADTITELLIRMKRAETYCPRPLLALDTTHDRRKQKIIAPEKQVLNFDLLKLAGDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRL 31-AUG-1995
                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary
Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FMDVAICP2 327 bp mRNA linear VRL 31-AUG-1
Foot and mouth disease virus Asia I mRNA for capsid protein
(partial) and protease (Mandya).
X88556
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2a protease; 2B protease; immunogenic protein; polyprotein; VP1
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<1. .>327
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Matches:
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/gene="VP1"
/product="VP1 protein"
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/product="2A protease"
322. .>37
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/product="2B
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/db_xref="SPTREMBL:067452"
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Foot and mouth disease virus 0 mRNA for capsid protein (partial)
              2 (bases 1 to 327)
Suryanarayana, V.V.S.
Direct Submission
Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary
Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
INDIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X88862.1 GI:971399
2a protease; 2B protease; immunogenic protein; polyprotein; VP1
gene; VP1 protein.
Foot-and-mouth disease virus.
Foot-and-mouth disease virus
Picornad-mouth positive-strand viruses; sRNA positive-strand viruses; proteins phthovirus.
1 (bases 1 to 330)
Suryanarayana,V.V.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary
Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singh,M., Mohan,B.M. and Suryanarayana,V.V.
Serological and molecular analysis of serotype O foot-and-mouth
disease virus isolated from disease outbreaks in India during
1987-91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .327
/organism="Foot-and-mouth disease virus"
/isolate="Asia I Nilgiri, Tamil Nadu"
/db_xref="taxon:12110"
/map="3337-3669 of 1D with 2A of FMDV"
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Matches:
Conservative:
Mismatches:
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/product="2A protease"
322. .>327
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274. .321
                                                                                                                                                                                                                                                                                                                                                                                                                    322. .>327
/product="2B protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-771-009-1 (1-17) x FMDVAICP3 (1-327)
                                                                                                                 Location/Qualifiers
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90.00
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96 c
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/gene="VP1"
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100.00%
100.00%
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of India
                                                                                                                                                                                                                                                                                                                              ESNPGPF
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DEFINITION
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VERSION
KEYWORDS
                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
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FMDV0CP02
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AUTHORS
TITLE
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AUTHORS
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JOURNAL
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                                                                                                                   FEATURES
                                                      TITLE
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/product="immunogenic polyprotein with 2A protease"
/protein_id="CAA61332.1"
/db_xref="G1:971400"
/db_xref="SPTREMBL:067432"
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YGAIKATGVTELPYRMPRAETYCPRPLLAIHPSEARHNEDCATLEQLLNFDLLKLAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2a protease; 2B protease; immunogenic protein; polyprotein; VP1 gene; VP1 protein.

gene; VP1 protein.

Foot-and-mouth disease virus.

Foot-and-mouth disease virus

Viruses; SSRNA positive-strand viruses, no DNA stage;

Picornaviridae; Aphthovirus.

1 (bases 1 to 330)

Tulastram, P., Tyagi, M. and Suryanarayana, V.

Antigenic variation in foot and mouth disease virus type Asia I
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Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary
Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Foot-and-mouth disease virus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Foot-and-mouth disease virus"
/isolate="A22 Tamil Nadu, India"
/db_xref="taxon:12110"
                                                                                                               /isolate="type O OEK"
/db_xref="taxon:12110"
/map="3337-3669 of 1D with 2A of FMDV"
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17
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Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                             /product="VP1 protein"
277, 324
                                                                                                                                                                                                                                                                                                                                                                                                                        /product="2A protease" 325. .>330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protease"
Virus Res. 43 (1), 45-55 (1996) 96419934
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                                                                                                                                                                                             /codon_start=1
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90.00
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/gene="VP1"
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100 c
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Unpublished
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VRL 31-AUG-1995
  AVRATTIHELLVRMKRAELYCPRPLIGSGGVVTRQKQTEDHCTNKQLLNFDLLKLAGD
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AVRATITHELLVRMKRAELYCPRPPIGSGGVVTRQTQTEDHCTSKQLLNFDLLKLAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 bp mRNA linear VRL 31-AUG-199. Foot and mouth disease virus A22 mRNA for capsid protein (partial) x88858
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Foot-and-mouth disease virus.

Viruses; ssRNA positive-strand viruses, no DNA stage;

Vicuses; Aphthovirus.

1 (bases; Aphthovirus.)

Tulasizam, P., Tyagi, M. and Suryanarayana, V.

Antigenic variation in foot and mouth disease virus type Asia I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary
Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
/product="immunogenic polyprotein with 2A protease"
/protein id="cases"
/db_xref="G1:971412"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /isolate="A22 vaccine strain (India)"
//db_xref="taxon:12110"
//map="337-3669 of 1D with 2A of FMDV"
//call_line="Baby Hamster Kidney (BHK)21 clone 13"
<1. .>330
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/organism="Foot-and-mouth disease virus"
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                      63
                                                                    /gene="VP1"
/groduct="VP1 protein"
277. .334
/product="22 protease"
325. .>330
/product="2B protease"
1. .276
/gene="VP1"
a 103 c 85 g (
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/product="vP1 protein"
277, .324
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/product="2A protease"
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                             VESNPGPF"
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                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
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FMDVAICP4
LOCUS
DEFINITION
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ORIGIN
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TITLE
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KEYWORDS
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                                                                       /product="immunogenic polyprotein with 2A protease"
/protein_id="CAA61330.1"
/protein_id="CAA61330.1"
/db_xref="SP1402"
/db_xref="SP37436"
/translation="APHRVLATVYTGTSKYPSAGRRRGDLGPLRQEDRRQLPASFNFG
AVRATTIHELLVRMKRAELXCPRPLIGSGGVVTRQTGGDGCTSKQLLNFDLLKLAGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FMDVA22CP 330 bp mRNA linear VRL 31-AUG-1995
Foot and mouth disease virus A22 mRNA for capsid protein (partial)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A protease; immunogenic protein; polyprotein; VP1 gene; VP1 protein.

gene; VP1 protein.

gene; VP1 protein.

Foot-and-mouth disease virus.

Foot-and-mouth disease virus.

Viruses; ssRNA positive-strand viruses, no DNA stage;

Viruses; ssRNA positive-strand viruses, no DNA stage;

Viruses; phthovirus.

1 (Dases I to 330)

Tulasiram, P., Tyagi, M. and Suryanarayana, V.

Antigenic variation in foot and mouth disease virus type Asia I isolates of India
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservation (Conservation of the Conservation of the Conservation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Foot-and-mouth disease virus"
/isolate="A22 Cuddapah, A.P. India"
/db.xref="taxon:12110"
/map="3337-3669 of 1D with 2A of FMDV"
/map="3337-3669 of 1D with 2A of FMDV"
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Matches:
Conservative:
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Indels:
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                                                                                                                                                                                                                                                                                                                277. .324
/product="2A protease"
325. .>330
                                                                                                                                                                                                                                                                                   /product="VP1 protein" 277. .324
                                                                                                                                                                                                                                                                                                                                                                                     325. .>330
/product="2B protease"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-771-009-1 (1-17) x FMDVA22C2 (1-330)
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                                                    /codon_start=1
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90.00
100.00%
100.00%
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/gene="VP1"
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                             .>330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                       gene
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TITLE
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AUTHORS
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JOURNAL
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                          CDS
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330 bp mRNA linear VRL 07-JAN-1997
Foot and mouth disease virus 0 mRNA for capsid protein (partial)
and protease (vaccine strain).
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YGAIKATRVTELLYRMKRAETYCPRPLLAIHPNEARHNEDCAPVKQLLNFDLLKLAGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 330)

Singh,M., Mohan,B.M. and Suryanarayana,V.V.

Serological and molecular analysis of serotype O foot-and-mouth

disease virus isolated from disease outbreaks in India during

1987-91
                                                                                                                                                                                                                                                                                                                           2a protease; 2B protease; immunogenic protein; polyprotein; VP1 gene; VP1 protein.
Foot-and-mouth disease virus.
Foot-and-mouth disease virus
Viruses; ssRNA positive-strand viruses picornaviridae; Aphthovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="immunogenic polyprotein with 2A protease"
/protein_id="CAA61333.1"
/db_xref="GI:971416"
/db_xref="SPTREMBL:Q67455"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .330
/organism="Foot-and-mouth disease virus"
/organism="Foot-and-mouth disease virus"
/orlate="taxon:12110"
/map="3337-3669 of 1D with 2A of FMDV"
/coll_line="Baby Hamster Kidney (BHK)21 clone
<1. .>330
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17
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                                          Length:
Matches:
Conservative:
Mismatches:
Indels:
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277. .324
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/product="2B
                                          2.46e-08
90.00
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/gene="VP1"
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                                                                      Percent Similarity:
Best Local Similarity:
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                             Alignment Scores:
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KEYWORDS
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                                                          Score:
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/product="immunogenic polyprotein with 2A protease"
/product="immunogenic polyprotein with 2A protease"
/db_xref="G1:971841"
/db_xref="G1:971841"
/db_xref="SPTR8H1:067454"
/translation="APHRVLASCYNGNCKYGDGTVTNIRGDQQVLAQKAARALPTSFN
YGAIRATRYTELLYRWKRAETYCPRPLIAIDPNEARHKEDCAPVKQLLNFDLLKLAGD
                                                                                                                                                                                                                                                                                                                              VRL 07-JAN-1997
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Singh, M, Mohan, B.M. and Suryanarayana, V.V.
Serological and molecular analysis of serotype O foot-and-mouth
disease virus isolated from disease outbreaks in India during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (20-JUN-1995) V.V.S. Suryanarayana, Indian Veterinary Research Institute, Scientist (SG), Hebbal, Bangalore 560 024,
                                                                                                                                                                                                                                       /organism="Foot-and-mouth disease virus"
.Yololate="type O Karnataka, India"
./db_xref="taxon:12110"
/map="3337-3669 of 1D with 2A of FMDV"
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Mismatches:
Indels:
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325. .>330
/product="2B protease"
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1. .276
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                                       /gene="VP1"
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US-09-771-009-1 (1-17) x AX364557 (1-873)
 GI:210468
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TITLE
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AX364557
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                                                                                                                                                                                        AF024509 493 bp RNA linear VRL 26-MAR-1998
Foot-and-mouth disease virus Asia-1 polyprotein gene, partial cds.
AF024509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"polyprotein"
/protein.id="AAC40617.1"
/db_xref="GI:2988471"
/translation-"LYHTGPYTWVPNGAPKTALDNQTNPTAYHKQPITRLALPYTAPH
RVLATYYNGKTYGEBPTMRCDCAVLASKYNKQLPFSFNYGAYKAENITEMILRIKRA
ETXCPRPLLALDTTQDRRKQEIIAPEKQLLNFDLLKLAGDVESNPGPFFFSDVRSNXT
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                                                                                                                                                                                                                                                                                                                                                           Detection and characterization of foot-and-mouth disease virus in
                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 493)
Bastos,A.D.S.
Bastos,A.D.S.
Submission
Submitted (10-SEP-1997) Research and Diagnostics, Onderstepoort
Institute for Exotic Diseases, Ou Soutpan Rd, Onderstepoort,
Pretoria, Gauteng 0110, South Africa
Location/Qualifiers
1. 493
                                                                                                                                 277 AACTTTGACCTGCTCAAGTTGGCGGGAGACGTGGAGTCCAACCCTGGGCCC 327
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                                                                                                              1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 others
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                                                                                                                                                                                                                                                                                                                                                                    Sub-Saharan Africa
Onderstepoort J. Vet. Res. 65 (1), 37-47 (1998)
982932334
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Foot-and-mouth disease virus
Viruses; ssRNA positive-strand viruses, no licornaviridae; Aphthovirus.

I (bases 1 to 493)
Bastos, A.D.
             Conservative:
Mismatches:
Indels:
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Mismatches:
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Matches:
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                                                        Gaps:
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                                                                                    US-09-771-009-1 (1-17) x FMDVOCP03 (1-330)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Asia-1
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/codon_start=3
                                                                                                                                                                                                                                            AF024509.1 GI:2988470
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             Percent Similarity:
Best Local Similarity:
Query Match:
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Best Local Similarity:
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AUTHORS
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AUTHORS
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PAT 15-FEB-2001
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The Dow Chemical Company (US) ; Reddy, S. Avutu (US) ; Larrinua, M. Ignacio (US) ; Ruegger, Max (US) ; Weglarz, Ted (US) ; Blakeslee, Beth (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reddy,S.A., Larrinua,M.I., Ruegger,M., Weglarz,T., Blakeslee,B., Orledo,V.B., Savickas,J.P., McCrery,A.D., Miller,A.B., Pogue,P.G. Della-Cioppa,R.G., Wolfe,M.G., Zheng,W., Gachotte,D., Grosley,R. and Pell,R.
vp1; vp1 capsid protein.

Proof and mouth disease virus, cDNA to viral RNA.

Foot-and-mouth disease virus

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Aphthovirus.

I (bases 1 to 750)

Beck, E. and Strohmaier, K.

Subtyping of European foot-and-mouth disease virus strains by nucleotide sequence determination

J. Virol. 61 (5), 1621-1629 (1987)

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1. .750
7. Organism="Foot-and-mouth disease virus"
7db_xref="taxon:12110"
1. .639
7note="VP1 capsid protein"
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               1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
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Aorganism="synthetic construct"
/db_stref="taxon:33630"
/note="nucleotide sequence of construct enh E6,
a 197 c 217 g 241 t
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              Regts, D.G., Wilschut, J.C., Holtrop, M. and Daemen, C.A. Genetic immunisation against cervical carcinoma Patent: EP 1195438-A 7 10-APR-2002; Rijksuniversiteit te Groningen (NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Regts, D.G., Holtrop, M., Wilschut, J.C. and Daemen, C.A. Genetic immunisation against cervical carcinoma Patent: WO 0229074-A 7 11-APR-2002; Rijksuniversiteit Groningen (NL)
1 AsnPheAspLeuLeuLysLeuAlaGlyAspValGluSerAsnProGlyPro 17
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AX460903
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/organism="Foot-and-mouth disease virus"
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Foot and mouth disease virus transgenic DNA.
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Foot-and-mouth disease virus
Viruses: SSRNA positive-strand viruses, no D
Picornaviridae; Aphthovirus.
1 (bases 1 to 961)
Nofschneider, P. H., Schaller, H., Kupper, H.A.
Patent: GB 2079288-A 2 20-JAN-1982;
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/gene="Vp1"
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